



SEQUENCE LISTING

<110> Bruck, Claudine
Bollen, Alex
Jacobs, Paul
Massaer, Marc

<120> Recombinant Allergen with Reduced
Enzymatic Activity

<130> B45122

<140> 09/554,860

<141> 2000-05-19

<150> PCT/EP98/07521

<151> 1998-11-16

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<223> Mutant of DerP1

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ggaggtgcca tcaaccattt gtccgatttg tcgttggatg aattcaaaaa ccgatttttg 240
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RECEIVED
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TECH CENTER 1600/2900

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Phe	Asn	Lys	Ser	Tyr	Ala	Thr	Phe	Glu	Asp	Glu	Glu	Ala	Ala	Arg	Lys	35	40	45	
Asn	Phe	Leu	Glu	Ser	Val	Lys	Tyr	Val	Gln	Ser	Asn	Gly	Gly	Ala	Ile	50	55	60	
Asn	His	Leu	Ser	Asp	Leu	Ser	Leu	Asp	Glu	Phe	Lys	Asn	Arg	Phe	Leu	65	70	75	80
Met	Ser	Ala	Glu	Ala	Phe	Glu	His	Leu	Lys	Thr	Gln	Phe	Asp	Leu	Asn	85	90	95	
Ala	Glu	Thr	Asn	Ala	Cys	Ser	Ile	Asn	Gly	Asn	Ala	Pro	Ala	Glu	Ile	100	105	110	
Asp	Leu	Arg	Gln	Met	Arg	Thr	Val	Thr	Pro	Ile	Arg	Met	Gln	Gly	Gly	115	120	125	
Cys	Gly	Ser	Ala	Trp	Ala	Phe	Ser	Gly	Val	Ala	Ala	Thr	Glu	Ser	Ala	130	135	140	

Tyr	Leu	Ala	Tyr	Arg	Asn	Gln	Ser	Leu	Asp	Leu	Ala	Glu	Gln	Glu	Leu
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Val	Asp	Cys	Ala	Ser	Gln	His	Gly	Cys	His	Gly	Asp	Thr	Ile	Pro	Arg
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Gly	Ile	Glu	Tyr	Ile	Gln	His	Asn	Gly	Val	Val	Gln	Glu	Ser	Tyr	Tyr
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Arg	Tyr	Val	Ala	Arg	Glu	Gln	Ser	Cys	Arg	Arg	Pro	Asn	Ala	Gln	Arg
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Phe	Gly	Ile	Ser	Asn	Tyr	Cys	Gln	Ile	Tyr	Pro	Pro	Asn	Val	Asn	Lys
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225					230					235					240
Gly	Ile	Lys	Asp	Leu	Asp	Ala	Phe	Arg	His	Tyr	Asp	Gly	Arg	Thr	Ile
				245					250						255
Ile	Gln	Arg	Asp	Asn	Gly	Tyr	Gln	Pro	Asn	Tyr	Ala	Ala	Val	Asn	Ile
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Ser	Trp	Asp	Thr	Asn	Trp	Gly	Asp	Asn	Gly	Tyr	Gly	Tyr	Phe	Ala	Ala
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aatggaaaatg ctccagctga aatcgatttg cgacaaatgc gaactgtcac tcccattcgt 360
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 ggtgtcgtcc aagaaagcta ctatcgatac gttgcacgag aacaatcatg cgcacgacca 600
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Tyr	Ala	Arg	Pro	Ser	Ser	Ile	Lys	Thr	Phe	Glu	Glu	Tyr	Lys	Lys	Ala
			20					25					30		
Phe	Asn	Lys	Ser	Tyr	Ala	Thr	Phe	Glu	Asp	Glu	Glu	Ala	Ala	Arg	Lys
	35						40					45			
Asn	Phe	Leu	Glu	Ser	Val	Lys	Tyr	Val	Gln	Ser	Asn	Gly	Gly	Ala	Ile
	50					55					60				
Asn	His	Leu	Ser	Asp	Leu	Ser	Leu	Asp	Glu	Phe	Lys	Asn	Arg	Phe	Leu
65					70					75				80	
Met	Ser	Ala	Glu	Ala	Phe	Glu	His	Leu	Lys	Thr	Gln	Phe	Asp	Leu	Asn
				85					90					95	
Ala	Cys	Ser	Ile	Asn	Gly	Asn	Ala	Pro	Ala	Glu	Ile	Asp	Leu	Arg	Gln
			100					105					110		
Met	Arg	Thr	Val	Thr	Pro	Ile	Arg	Met	Gln	Gly	Gly	Cys	Gly	Ser	Cys
	115						120					125			
Trp	Ala	Phe	Ser	Gly	Val	Ala	Ala	Thr	Glu	Ser	Ala	Tyr	Leu	Ala	Tyr
	130					135					140				
Arg	Asn	Gln	Ser	Leu	Asp	Leu	Ala	Glu	Gln	Glu	Leu	Val	Asp	Cys	Ala
145					150					155				160	

Ser	Gln	His	Gly	Cys	His	Gly	Asp	Thr	Ile	Pro	Arg	Gly	Ile	Glu	Tyr			
					165					170				175				
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					180					185				190				
Arg	Glu	Gln	Ser	Cys	Arg	Arg	Pro	Asn	Ala	Gln	Arg	Phe	Gly	Ile	Ser			
					195					200				205				
Asn	Tyr	Cys	Gln	Ile	Tyr	Pro	Pro	Asn	Val	Asn	Lys	Ile	Arg	Glu	Ala			
					210					215				220				
Leu	Ala	Gln	Thr	His	Ser	Ala	Ile	Ala	Val	Ile	Ile	Gly	Ile	Lys	Asp			
					225					230				235				240
Leu	Asp	Ala	Phe	Arg	His	Tyr	Asp	Gly	Arg	Thr	Ile	Ile	Gln	Arg	Asp			
					245					250				255				
Asn	Gly	Tyr	Gln	Pro	Asn	Tyr	His	Ala	Val	Asn	Ile	Val	Gly	Tyr	Ser			
					260					265				270				
Asn	Ala	Gln	Gly	Val	Asp	Tyr	Trp	Ile	Val	Arg	Asn	Ser	Trp	Asp	Thr			
					275					280				285				
Asn	Trp	Gly	Asp	Asn	Gly	Tyr	Gly	Tyr	Phe	Ala	Ala	Asn	Ile	Asp	Leu			
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ggaggtgcc	tcaaccattt	gtccgatttg	tcgttggtatg	aattcaaaaa	ccgatttttg	240
atgagtgcag	aagcttttga	acacctcaaa	actcaattcg	atttgaatgc	tgaaactaac	300
gcctgcagta	tcaatggaaa	tgctccagct	gaaatcgatt	tgcgacaaat	gcgaactgtc	360
actcccatc	gtatgcaagg	aggctgtggt	tcacgatggg	ctttctctgg	tgttgccgca	420
actgaatcag	cttatttggc	ttaccgtaat	caatcattgg	atcttgctga	acaagaatta	480
gtcgattgtg	cttcccaaca	cggttgtcat	ggtgatacca	ttccacgtgg	tattgaatac	540

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			20					25					30		
Phe	Asn	Lys	Ser	Tyr	Ala	Thr	Phe	Glu	Asp	Glu	Glu	Ala	Ala	Arg	Lys
	35						40					45			
Asn	Phe	Leu	Glu	Ser	Val	Lys	Tyr	Val	Gln	Ser	Asn	Gly	Gly	Ala	Ile
	50					55					60				
Asn	His	Leu	Ser	Asp	Leu	Ser	Leu	Asp	Glu	Phe	Lys	Asn	Arg	Phe	Leu
65					70				75					80	
Met	Ser	Ala	Glu	Ala	Phe	Glu	His	Leu	Lys	Thr	Gln	Phe	Asp	Leu	Asn
				85					90					95	
Ala	Glu	Thr	Asn	Ala	Cys	Ser	Ile	Asn	Gly	Asn	Ala	Pro	Ala	Glu	Ile
			100					105					110		
Asp	Leu	Arg	Gln	Met	Arg	Thr	Val	Thr	Pro	Ile	Arg	Met	Gln	Gly	Gly
	115						120						125		
Cys	Gly	Ser	Ala	Trp	Ala	Phe	Ser	Gly	Val	Ala	Ala	Thr	Glu	Ser	Ala
	130					135					140				
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145					150					155				160	
Val	Asp	Cys	Ala	Ser	Gln	His	Gly	Cys	His	Gly	Asp	Thr	Ile	Pro	Arg
				165					170					175	

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		180						185					190		
Arg	Tyr	Val	Ala	Arg	Glu	Gln	Ser	Cys	Arg	Arg	Pro	Asn	Ala	Gln	Arg
		195					200					205			
Phe	Gly	Ile	Ser	Asn	Tyr	Cys	Gln	Ile	Tyr	Pro	Pro	Asn	Val	Asn	Lys
		210				215				220					
Ile	Arg	Glu	Ala	Leu	Ala	Gln	Thr	His	Ser	Ala	Ile	Ala	Val	Ile	Ile
225				230						235				240	
Gly	Ile	Lys	Asp	Leu	Asp	Ala	Phe	Arg	His	Tyr	Asp	Gly	Arg	Thr	Ile
			245					250					255		
Ile	Gln	Arg	Asp	Asn	Gly	Tyr	Gln	Pro	Asn	Tyr	Ala	Ala	Val	Asn	Ile
		260					265						270		
Val	Gly	Tyr	Ser	Asn	Ala	Gln	Gly	Val	Asp	Tyr	Trp	Ile	Val	Arg	Asn
		275				280						285			
Ser	Trp	Asp	Thr	Asn	Trp	Gly	Asp	Asn	Gly	Tyr	Gly	Tyr	Phe	Ala	Ala
	290					295					300				
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		20					25				30				
Ala	His	Ser	Ala	Phe	Ala	Ala	Asp	Pro	Arg	Pro	Ser	Ser	Ile	Lys	Thr
	35					40					45				
Phe	Glu	Glu	Tyr	Lys	Lys	Ala	Phe	Asn	Lys	Ser	Tyr	Ala	Thr	Phe	Glu
	50					55				60					
Asp	Glu	Glu	Ala	Ala	Arg	Lys	Asn	Phe	Leu	Glu	Ser	Val	Lys	Tyr	Val
65				70						75				80	

Gln Ser Asn Gly Gly Ala Ile Asn His Leu Ser Asp Leu Ser Leu Asp			
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Glu Phe Lys Asn Arg Phe Leu Met Ser Ala Glu Ala Phe Glu His Leu			
	100	105	110
Lys Thr Gln Phe Asp Leu Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro			
	115	120	125
Ala Glu Ile Asp Leu Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met			
	130	135	140
Gln Gly Gly Cys Gly Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr			
	145	150	155
Glu Ser Ala Tyr Leu Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu			
	165	170	175
Gln Glu Leu Val Asp Cys Ala Ser Gln His Gly Cys His Gly Asp Thr			
	180	185	190
Ile Pro Arg Gly Ile Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu			
	195	200	205
Ser Tyr Tyr Arg Tyr Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn			
	210	215	220
Ala Gln Arg Phe Gly Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn			
	225	230	235
Ala Asn Lys Ile Arg Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala			
	245	250	255
Val Ile Ile Gly Ile Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly			
	260	265	270
Arg Thr Ile Ile Gln Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala			
	275	280	285
Val Asn Ile Val Gly Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile			
	290	295	300
Val Arg Asn Ser Trp Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr			
	305	310	315
Phe Ala Ala Asn Ile Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val			
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			20					25					30		
Ala	His	Ser	Ala	Phe	Ala	Ala	Asp	Pro	Arg	Pro	Ser	Ser	Ile	Lys	Thr
			35				40					45			
Phe	Glu	Glu	Tyr	Lys	Lys	Ala	Phe	Asn	Lys	Ser	Tyr	Ala	Thr	Phe	Glu
	50					55					60				
Asp	Glu	Glu	Ala	Ala	Arg	Lys	Asn	Phe	Leu	Glu	Ser	Val	Lys	Tyr	Val
65					70					75					80
Gln	Ser	Asn	Gly	Gly	Ala	Ile	Asn	His	Leu	Ser	Asp	Leu	Ser	Leu	Asp
				85					90					95	
Glu	Phe	Lys	Asn	Arg	Phe	Leu	Met	Ser	Ala	Glu	Ala	Phe	Glu	His	Leu
			100					105					110		
Lys	Thr	Gln	Phe	Asp	Leu	Asn	Ala	Glu	Thr	Asn	Ala	Cys	Ser	Ile	Asn
		115					120					125			
Gly	Asn	Ala	Pro	Ala	Glu	Ile	Asp	Leu	Arg	Gln	Met	Arg	Thr	Val	Thr
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Pro	Ile	Arg	Met	Gln	Gly	Gly	Cys	Gly	Ser	Ala	Trp	Ala	Phe	Ser	Gly
145					150					155					160
Val	Ala	Ala	Thr	Glu	Ser	Ala	Tyr	Leu	Ala	Tyr	Arg	Asn	Gln	Ser	Leu
				165					170					175	
Asp	Leu	Ala	Glu	Gln	Glu	Leu	Val	Asp	Cys	Ala	Ser	Gln	His	Gly	Cys
			180					185					190		
His	Gly	Asp	Thr	Ile	Pro	Arg	Gly	Ile	Glu	Tyr	Ile	Gln	His	Asn	Gly
		195					200					205			
Val	Val	Gln	Glu	Ser	Tyr	Tyr	Arg	Tyr	Val	Ala	Arg	Glu	Gln	Ser	Cys
	210						215					220			
Arg	Arg	Pro	Asn	Ala	Gln	Arg	Phe	Gly	Ile	Ser	Asn	Tyr	Cys	Gln	Ile
225					230					235					240
Tyr	Pro	Pro	Asn	Ala	Asn	Lys	Ile	Arg	Glu	Ala	Leu	Ala	Gln	Thr	His
				245					250					255	
Ser	Ala	Ile	Ala	Val	Ile	Ile	Gly	Ile	Lys	Asp	Leu	Asp	Ala	Phe	Arg
			260					265						270	

His Tyr Asp Gly Arg Thr Ile Ile Gln Arg Asp Asn Gly Tyr Gln Pro
 275 280 285
 Asn Tyr His Ala Val Asn Ile Val Gly Tyr Ser Asn Ala Gln Gly Val
 290 295 300
 Asp Tyr Trp Ile Val Arg Asn Ser Trp Asp Thr Asn Trp Gly Asp Asn
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 Gly Tyr Gly Tyr Phe Ala Ala Asn Ile Asp Leu Met Met Ile Glu Glu
 325 330 335
 Tyr Pro Tyr Val Val Ile Leu
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attagctgct ccaactaacg cctgca 86

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aggaaatctc atcgtttg 78

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tttgaacgcc tgca 74

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<223> Primer

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66

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<223> Primer

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25

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cggtttttga attcatccaa cgac

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<212> DNA

<213> Artificial Sequence

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<212> DNA

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17

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Asn Ala Glu Thr

1